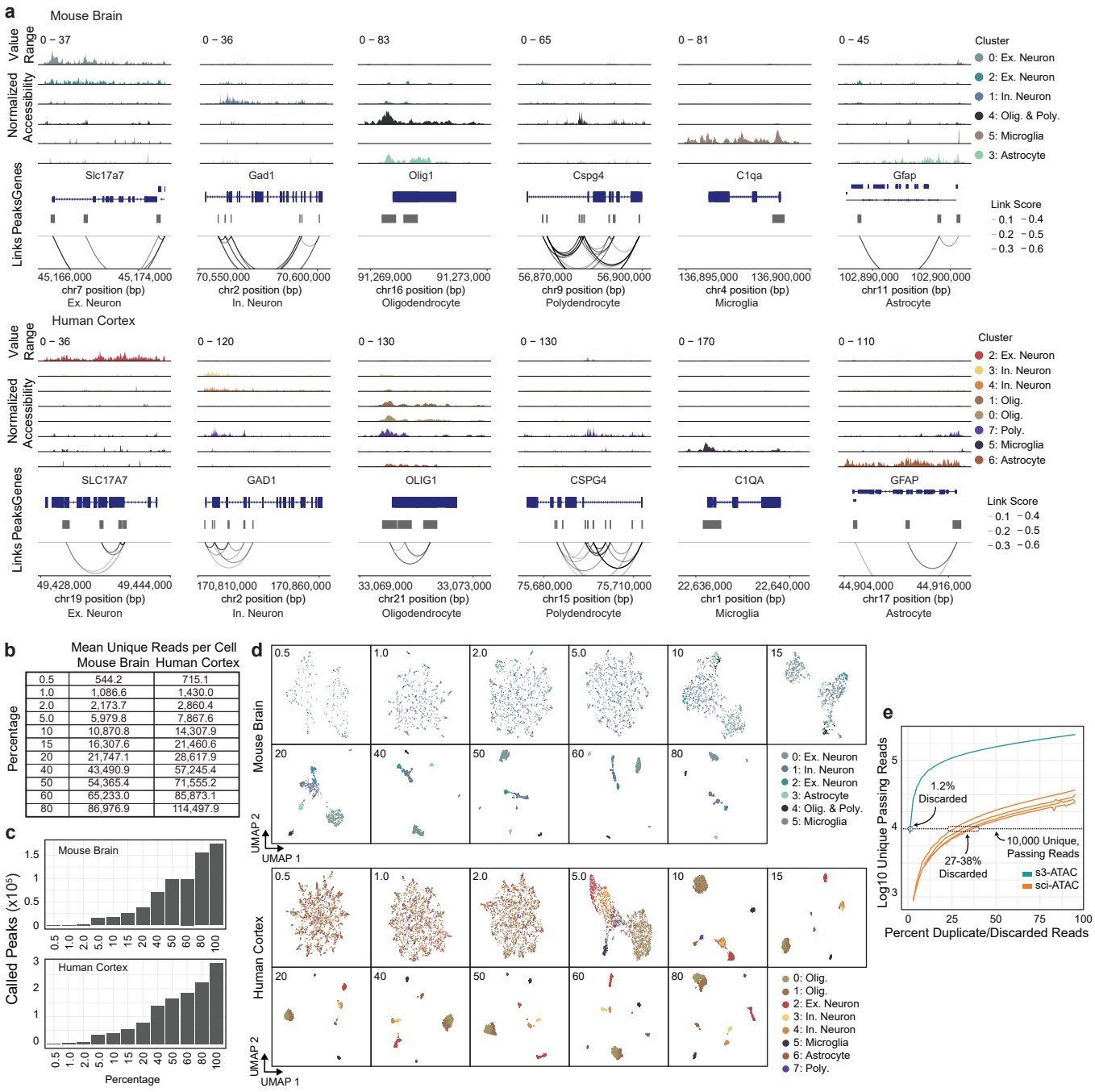
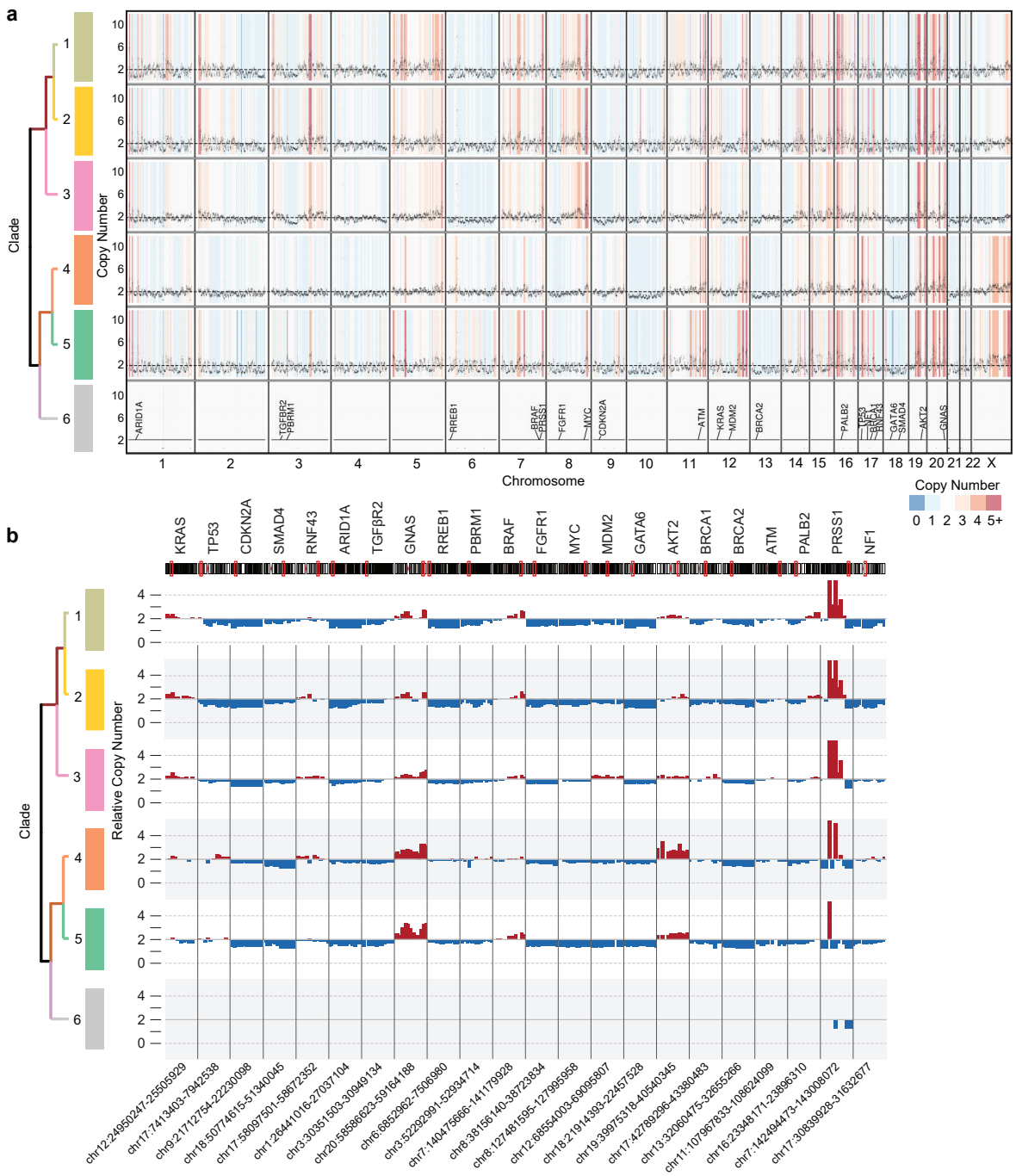
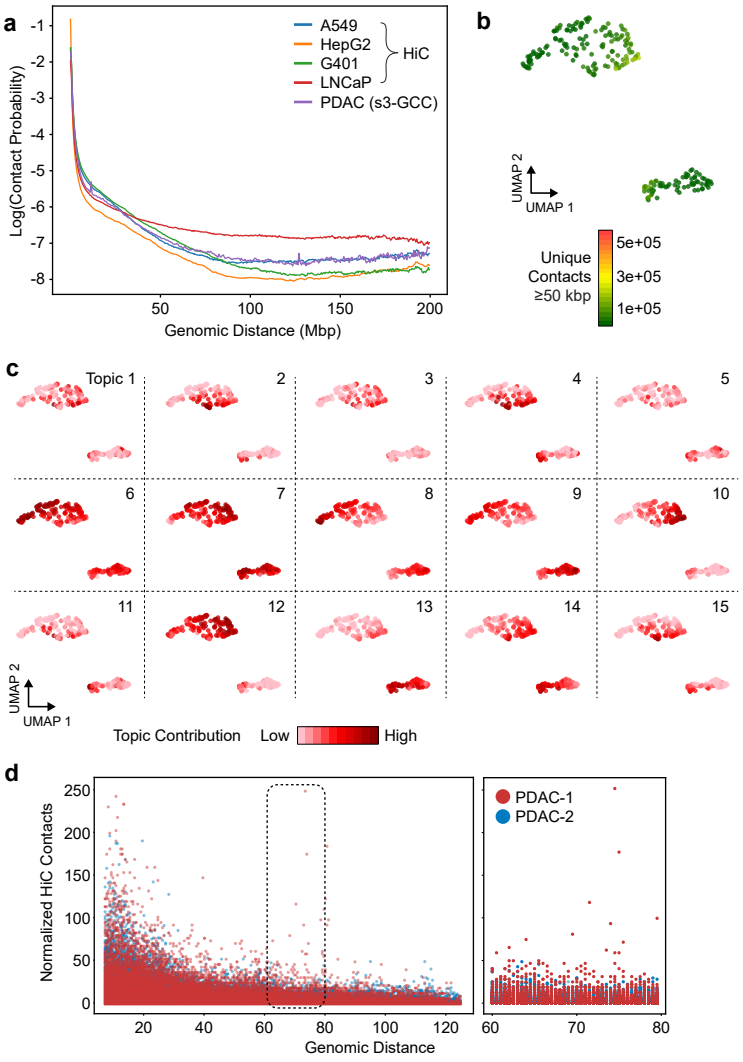


Percentage	Mouse Brain	Human Cortex
0.5	544.2	715.1
1.0	1,086.6	1,430.0
2.0	2,173.7	2,860.4
5.0	5,979.8	7,867.6
10	10,870.8	14,307.9
15	16,307.6	21,460.6
20	21,747.1	28,617.9
40	43,490.9	57,245.4
50	54,365.4	71,555.2
60	65,233.0	85,873.1
80	86,976.9	114,497.9

Supplementary Figure 1 | Marker sets for gross cell type discrimination in human cortex and mouse whole brain data sets and down sampling analysis. (a) Genome coverage plots of marker genes for mouse (top) and human (bot.) cell types. Cells are separated into tracks based on clustering and signal aggregated. (b) Table of down sampling analysis percentages (percentage of reads per cell) and mean unique reads per cell. (c) Number of called peaks for down sampled data for mouse (top) and human (bot.). (d) UMAPs of cells colored by full data set cluster identity for down sampled data on mouse (top) and human (bot.). Percentage of reads used per cell is listed in the top corner of each subpanel. (e) Log10 unique, passing reads as a function of library saturation for s3-ATAC and sci-ATAC datasets. Dashed line represents 10,000 unique passing reads, with the percentage of total reads discarded for each method to achieve that total.



Supplementary Figure 2 | Pseudo-bulk whole genome copy number calling. (a) Pseudo-bulk genome-wide relative copy number calling. Scatter plot of reads per bin (50 kbp) separated by clade and chromosome. Clade assignment shown on left and relate to Figure 5b (k=6). Recurrently mutated gene locations in PDAC25 highlighted along the read count bins for clade 6. Shading of plot colored by relative copy number in genomic locus. (b) Select genes with known copy number aberrations in PDAC bar plot for relative copy number per clade. Middle line per row is copy number neutral, amplifications in red and deletions in blue. Red boxes on chromosome ideograms at the top of each window indicate the position of the gene.



Supplementary Figure 3 | Clustering of s3GCC profiles. (a) Contact probability as function of genomic distance for s3-GCC data compared to bulk HiC datasets. (b) Unique contacts ≥50 kbp displayed on UMAP dimensions for quality control purposes. (c) Topic contribution scores plotted over UMAP projection of s3-GCC cells. (d) Normalized HiC contacts for PDAC-1 and PDAC-2 cell lines for chromosome 12, windows within the translocation specific to PDAC-1 exhibit elevated HiC contacts comparable to much shorter distances (<20 Mbp).